

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Examiner : Not yet assigned  
Group : Not yet assigned  
Applicants : Jens Kossmann et al.  
Serial No. : Not yet assigned  
Filed : Concurrently herewith  
For : NUCLEIC ACID MOLECULES CODING FOR  
DEBRANCHING ENZYMES FROM MAIZE

New York, New York  
May 8, 2001

Hon. Commissioner for Patents  
Washington, D.C. 20231

**STATEMENTS IN SUPPORT OF AMENDMENTS TO  
SEQUENCE LISTING UNDER 37 C.F.R. § 1.825(a)  
AND IN SUPPORT OF COMPUTER READABLE  
FORM SUBMISSION UNDER 37 C.F.R. § 1.821(e)**

Sir:

In accordance with 37 C.F.R. § 1.825(a), I hereby state that the paper copy of the Sequence Listing enclosed herewith does not include new matter and is supported by the application as originally filed.

I also hereby state, in accordance with 37 C.F.R. § 1.821(e), that the content of the Computer Readable Form copy of the Sequence Listing submitted with the September 4, 1998 Preliminary Amendment in United States application no.

09/148,680 and the above-mentioned paper copy of the substitute Sequence Listing is  
the same.

Respectfully submitted,



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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: PlantTec Biotechnologie GmbH Forschung & Entwicklung
- (B) STREET: Hermannswerder 14
- (C) CITY: Potsdam
- (E) COUNTRY: Germany
- (F) POSTAL CODE: 14473

(ii) TITLE OF THE INVENTION: Nucleic acid molecules coding for debranching enzymes from maize

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER-READABLE VERSION:

- (A) DATA CARRIER: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Zea mays
- (F) TISSUE TYPE: Blattgewebe

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGC ACG AGG TCA AAA CTC CCT CCA GGG TCA GAT TTG CAA CAA GCT GCA	48
Gly Thr Arg Ser Lys Leu Pro Pro Gly Ser Asp Leu Gln Gln Ala Ala	
1 5 10 15	
ATT GTG GCT ATT CAG GAA GAG GAC CCT TAT AAT TGG GGG TAT AAC CCT	96
Ile Val Ala Ile Gln Glu Asp Pro Tyr Asn Trp Gly Tyr Asn Pro	
20 25 30	
GTG GTT TGG GGC GTT CCA AAA GGA AGC TAT GCA AGT AAC CCA GAT GGT	144
Val Val Trp Gly Val Pro Lys Gly Ser Tyr Ala Ser Asn Pro Asp Gly	
35 40 45	

CCA AGT CGT ATC ATT GAG TAC CCG CTG ATG GTG CAG GCC TTG AAT CGC Pro Ser Arg Ile Ile Glu Tyr Arg Leu Met Val Gln Ala Leu Asn Arg	50	55	60	192
TTA GGT CTT CGA GTT GTC ATG GAT GTT GTA TAC AAT CAT CTA TAC TCA Leu Gly Leu Arg Val Val Met Asp Val Val Tyr Asn His Leu Tyr Ser	65	70	75	80
AGT GGC CCT TTT GCC ATC ACT TCC GTG CTT GAC AAG ATT GTA CCT GGA Ser Gly Pro Phe Ala Ile Thr Ser Val Leu Asp Lys Ile Val Pro Gly	85	90	95	288
TAC TAC CTC AGA AGG GAC TCT AAT GGT CAG ACT GAG AAC AGC GCG GCT Tyr Tyr Leu Arg Arg Asp Ser Asn Gly Gln Thr Glu Asn Ser Ala Ala	100	105	110	336
GTG AAC AAT ACA GCA AGT GAG CAT TTC ATG GTT GAT AGA TTA ATC GTG Val Asn Asn Thr Ala Ser Glu His Phe Met Val Asp Arg Leu Ile Val	115	120	125	384
GAT GAC CTT CTG AAT TGG GCA GTA AAT TAC AAA GTT GAC GGG TTC AGA Asp Asp Leu Leu Asn Trp Ala Val Asn Tyr Lys Val Asp Gly Phe Arg	130	135	140	432
TTT GAT CTA ATG GGA CAT ATC ATG AAA AAG ACA ATG ATT AGA GCA AAA Phe Asp Leu Met Gly His Ile Met Lys Lys Thr Met Ile Arg Ala Lys	145	150	155	160
TCG GCT CTT CAA AGC CTT ACA ATT GAT GAA CAT GGA GTA GAT GGT TCA Ser Ala Leu Gln Ser Leu Thr Ile Asp Glu His Gly Val Asp Gly Ser	165	170	175	528
AAG ATA TAC TTG TAT GGT GAA GGA TGG AAC TTC GGT GAA GTT GCG GAA Lys Ile Tyr Leu Tyr Gly Glu Gly Trp Asn Phe Gly Glu Val Ala Glu	180	185	190	576
AAT CAA CGT GGG ATA AAT GGA TCC CAG CTA AAT ATG AGT GGC ACT GGG Asn Gln Arg Gly Ile Asn Gly Ser Gln Leu Asn Met Ser Gly Thr Gly	195	200	205	624
ATT GGT AGT TTC AAC GAT AGA ATC CGT GAT GCT ATA AAT GGT GGC AGT Ile Gly Ser Phe Asn Asp Arg Ile Arg Asp Ala Ile Asn Gly Gly Ser	210	215	220	672
CCG TTT GGG AAT CCA CTG CAA CAA GGT TTC TCT ACT GGA TTG TTC TTA Pro Phe Gly Asn Pro Leu Gln Gln Gly Phe Ser Thr Gly Leu Phe Leu	225	230	235	720
GAG CCA AAT GGA TTT TAT CAG GGC AAT GAA ACA GAG ACA AGG CTC ACG Glu Pro Asn Gly Phe Tyr Gln Gly Asn Glu Thr Glu Thr Arg Leu Thr	245	250	255	768
CTT GCT ACA TAC GCT GAC CAT ATA CAG ATT GGA TTA GCT GGC AAT TTG Leu Ala Thr Tyr Ala Asp His Ile Gln Ile Gly Leu Ala Gly Asn Leu	260	265	270	816
AAG GAC TAT GTA GTT ATA TCT CAT ACT GGA GAA GCT AGA AAA GGA TCT Lys Asp Tyr Val Val Ile Ser His Thr Gly Glu Ala Arg Lys Gly Ser	275	280	285	864

GAA ATT CGC ACC TTC GAT GGC TCA CCA GTT GGC TAT GCT TCA TCC CCT Glu Ile Arg Thr Phe Asp Gly Ser Pro Val Gly Tyr Ala Ser Ser Pro 290 295 300	912
ATA GAA ACA ATA AAC TAC GCC TCT GCT CAT GAC AAT GAA ACA CTA TTT Ile Glu Thr Ile Asn Tyr Ala Ser Ala His Asp Asn Glu Thr Leu Phe 305 310 315 320	960
GAT ATT ATT AGT CTA AAG ACT CCG ATG GAC CTC TCA ATT GAC GAG CGA Asp Ile Ile Ser Leu Lys Thr Pro Met Asp Leu Ser Ile Asp Glu Arg 325 330 335	1008
TGC AGG ATA AAT CAT TTG TCC ACA AGC ATG ATT GCA TTA TCC CAG CGA Cys Arg Ile Asn His Leu Ser Thr Ser Met Ile Ala Leu Ser Gln Gly 340 345 350	1056
ATA CCA TTT TTT CAT GCT GGT GAT GAG ATA CTA CGA TCT AAG TCG CTT Ile Pro Phe Phe His Ala Gly Asp Glu Ile Leu Arg Ser Lys Ser Leu 355 360 365	1104
GAT CGA GAT TCA TAT GAC TCT GGT GAT TGG TTT AAC AAG ATT GAT TTT Asp Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Lys Ile Asp Phe 370 375 380	1152
ACC TAT GAA ACA AAC AAT TGG GGT GTT GGG CTT CCA CCA AGA GAA AAG Thr Tyr Glu Thr Asn Asn Trp Gly Val Gly Leu Pro Pro Arg Glu Lys 385 390 395 400	1200
AAC GAA GGG AGC TGG CCT TTG ATG AAG CCA AGA TTG GAG AAC CCG TCG Asn Glu Gly Ser Trp Pro Leu Met Lys Pro Arg Leu Glu Asn Pro Ser 405 410 415	1248
TTC AAA CCT GCA AAA CAT GAC ATT ATT GCT GCC TTA GAC AAA TTT ATT Phe Lys Pro Ala Lys His Asp Ile Ile Ala Leu Asp Lys Phe Ile 420 425 430	1296
GAT ATC CTC AAG ATC AGA TAC TCA TCA CCT CTC TTT CGC CTA ACT ACA Asp Ile Leu Lys Ile Arg Tyr Ser Ser Pro Leu Phe Arg Leu Thr Thr 435 440 445	1344
GCA AGT GAT ATT GTG CAA AGG GTT CAC TTT CAC AAC ACA GGG CCC TCC Ala Ser Asp Ile Val Gln Arg Val His Phe His Asn Thr Gly Pro Ser 450 455 460	1392
TTG GTT CCA GGA GTT ATT GTC ATG AGC ATC GAA GAT GCA CGA AAT GAT Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp 465 470 475 480	1440
AGG CAT GAT ATG GCC CAG ATA GAT GAA ACA TTC TCT TGT GTC GTT ACA Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr 485 490 495	1488
GTC TTC AAT GTA TGT CCG TAC GAA GTG TCT ATA GAA ATC CCT GAT CTT Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu 500 505 510	1536
GCA TCA CTG CGG CTT CAG TTG CAT CCA GTG CAG GTG AAT TCA TCG GAT Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp 515 520 525	1584

GCG TTA GCC AGG CAG TCT GCG TAC GAC ACC GCC ACA GGT CGA TTC ACC	1632
Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr	
530 535 540	
GTG CCG AAA AGG ACA GCA GCA GTG TTC GTG GAA CCC AGG TGC T	1675
Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys	
545 550 555	
GATGGATGCC TTTCGCTAGC GAGCAAGTGC ATTCCGGCATC CAAGTCGAAG CAAACGAATG	1735
AAATAAGAGA AGGCCATCGA ATAAAACGAA GTATATAAAT AGATTGAATA AGACGTTGCC	1795
CAAGTTGCCA AGGCACGCTT TGCCATATGT ATGCGTTGAA AAATAAATAA ATAATAAAT	1855
AAATGATGTT ATAGAGGTAC AAAAGCATTG GAACATTTCT TTATAGAGGT GAACCACCCCT	1915
ATTTTCCAGT TTCCATGTGT GAATTGTGAT TAGCATATGT ATGGAATAAT AATATAAATT	1975
AATTTTATGC AAAAAAAA	1993

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gly Thr Arg Ser Lys Leu Pro Pro Gly Ser Asp Leu Gln Gln Ala Ala  
1 5 10 15

Ile Val Ala Ile Gln Glu Glu Asp Pro Tyr Asn Trp Gly Tyr Asn Pro  
20 25 30

Val Val Trp Gly Val Pro Lys Gly Ser Tyr Ala Ser Asn Pro Asp Gly  
35 40 45

Pro Ser Arg Ile Ile Glu Tyr Arg Leu Met Val Gln Ala Leu Asn Arg  
50 55 60

Leu Gly Leu Arg Val Val Met Asp Val Val Tyr Asn His Leu Tyr Ser  
65 70 75 80

Ser Gly Pro Phe Ala Ile Thr Ser Val Leu Asp Lys Ile Val Pro Gly  
85 90 95

Tyr Tyr Leu Arg Arg Asp Ser Asn Gly Gln Thr Glu Asn Ser Ala Ala  
100 105 110

Val Asn Asn Thr Ala Ser Glu His Phe Met Val Asp Arg Leu Ile Val  
115 120 125

Asp Asp Leu Leu Asn Trp Ala Val Asn Tyr Lys Val Asp Gly Phe Arg  
130 135 140

Phe Asp Leu Met Gly His Ile Met Lys Lys Thr Met Ile Arg Ala Lys  
 145 150 155 160  
 Ser Ala Leu Gln Ser Leu Thr Ile Asp Glu His Gly Val Asp Gly Ser  
 165 170 175  
 Lys Ile Tyr Leu Tyr Gly Glu Gly Trp Asn Phe Gly Glu Val Ala Clu  
 180 185 190  
 Asn Gln Arg Gly Ile Asn Gly Ser Gln Leu Asn Met Ser Gly Thr Gly  
 195 200 205  
 Ile Gly Ser Phe Asn Asp Arg Ile Arg Asp Ala Ile Asn Gly Gly Ser  
 210 215 220  
 Pro Phe Gly Asn Pro Leu Gln Gln Gly Phe Ser Thr Gly Leu Phe Leu  
 225 230 235 240  
 Glu Pro Asn Gly Phe Tyr Gln Gly Asn Glu Thr Glu Thr Arg Leu Thr  
 245 250 255  
 Leu Ala Thr Tyr Ala Asp His Ile Gln Ile Gly Leu Ala Gly Asn Leu  
 260 265 270  
 Lys Asp Tyr Val Val Ile Ser His Thr Gly Glu Ala Arg Lys Gly Ser  
 275 280 285  
 Glu Ile Arg Thr Phe Asp Gly Ser Pro Val Gly Tyr Ala Ser Ser Pro  
 290 295 300  
 Ile Glu Thr Ile Asn Tyr Ala Ser Ala His Asp Asn Glu Thr Leu Phe  
 305 310 315 320  
 Asp Ile Ile Ser Leu Lys Thr Pro Met Asp Leu Ser Ile Asp Glu Arg  
 325 330 335  
 Cys Arg Ile Asn His Leu Ser Thr Ser Met Ile Ala Leu Ser Gln Gly  
 340 345 350  
 Ile Pro Phe Phe His Ala Gly Asp Glu Ile Leu Arg Ser Lys Ser Leu  
 355 360 365  
 Asp Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Lys Ile Asp Phe  
 370 375 380  
 Thr Tyr Glu Thr Asn Asn Trp Gly Val Gly Leu Pro Pro Arg Glu Lys  
 385 390 395 400  
 Asn Glu Gly Ser Trp Pro Leu Met Lys Pro Arg Leu Glu Asn Pro Ser  
 405 410 415  
 Phe Lys Pro Ala Lys His Asp Ile Ile Ala Ala Leu Asp Lys Phe Ile  
 420 425 430  
 Asp Ile Leu Lys Ile Arg Tyr Ser Ser Pro Leu Phe Arg Leu Thr Thr  
 435 440 445  
 Ala Ser Asp Ile Val Gln Arg Val His Phe His Asn Thr Cys Pro Ser  
 450 455 460

Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp  
 465 470 475 480

Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr  
 485 490 495

Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu  
 500 505 510

Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp  
 515 520 525

Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr  
 530 535 540

Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys  
 545 550 555

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE DESCRIPTION:
  - (A) LENGTH: 492 base pairs
  - (B) TYPE: nucleotide
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Solanum tuberosum
  - (B) STRAIN: Berolina
  - (F) TISSUE TYPE: tuber
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LAGE:1..492
  - (D) OTHER INFORMATION:/product= "debranching enzyme  
(R-enzyme)"

(xi) SEQUENCE INFORMATION: SEQ ID NO: 3:

TCT GCT GAT GGC AAG TGG ACA TTA TTA GTT AAT CTT GAT TCT GAT GAT	48
Ser Ala Asp Gly Lys Trp Thr Leu Leu Val Asn Leu Asp Ser Asp Asp	
560 565 570	
GTA AAA CCT GAA GGC TGG GAT AAT CTA CAA GAC GTG AAG CCA AAT CTT	96
Val Lys Pro Glu Gly Trp Asp Asn Leu Gln Asp Val Lys Pro Asn Leu	
575 580 585 590	
CTT TCC TTT TCT GAT GTC AGC ATC TAT GAG CTG CAT GTT AGA GAT TTC	144
Leu Ser Phe Ser Asp Val Ser Ile Tyr Glu Leu His Val Arg Asp Phe	
595 600 605	

ACT GCC AGT GAC CCT ACT GTG TCT CAT GAA TTT CAG GCC GGT TAT CTC		192
Thr Ala Ser Asp Pro Thr Val Ser His Glu Phe Gln Ala Gly Tyr Leu		
610	615	620
GCC CCT TCC ACG TCG CAG GCA TCA GCT GGT GTC CAA CAT TTG AAA AGA		240
Ala Pro Ser Thr Ser Gln Ala Ser Ala Gly Val Gln His Leu Lys Arg		
625	630	635
TTA TCA AGT GCT GGT ATC ACT CAT GTC CAC CTG TGG CCA ACC TAT CAA		288
Leu Ser Ser Ala Gly Ile Thr His Val His Leu Trp Pro Thr Tyr Gln		
640	645	650
TTT GCT GGT GTC GAA GAT GAG AAA CAT AAA TGG AAG TAT ACA GAT ATC		336
Phe Ala Gly Val Glu Asp Glu Lys His Lys Trp Lys Tyr Thr Asp Ile		
655	660	665
GAG AAA CTC AAC TCT TTT CCA CCA GAT TCT GAG GAG CAG CAG GCT CTT		384
Glu Lys Leu Asn Ser Phe Pro Pro Asp Ser Glu Glu Gln Gln Ala Leu		
675	680	685
ATC ACA GCC ATC CAA GAT GAA GAT GGC TAT AAT TGG GGG TAT AAT CCT		432
Ile Thr Ala Ile Gln Asp Glu Asp Gly Tyr Asn Trp Gly Tyr Asn Pro		
690	695	700
GTT CTC TGG GGA GTT CCA AAG GGA AGC TAT GCT GGT AAT GCA AAT GGT		480
Val Leu Trp Gly Val Pro Lys Gly Ser Tyr Ala Gly Asn Ala Asn Gly		
705	710	715
CCT TGT CGT ATC		492
Pro Cys Arg Ile		
720		

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ser Ala Asp Gly Lys Trp Thr Leu Leu Val Asn Leu Asp Ser Asp Asp  
 1 5 10 15

Val Lys Pro Glu Gly Trp Asp Asn Leu Gln Asp Val Lys Pro Asn Leu  
 20 25 30

Leu Ser Phe Ser Asp Val Ser Ile Tyr Glu Leu His Val Arg Asp Ile  
 35 40 45

Thr Ala Ser Asp Pro Thr Val Ser His Glu Phe Gln Ala Gly Tyr Leu  
 50 55 60

Ala Pro Ser Thr Ser Gln Ala Ser Ala Gly Val Gln His Leu Lys Arg  
 65 70 75 80

Leu Ser Ser Ala Gly Ile Thr His Val His Leu Trp Pro Thr Tyr Gln  
85 90 95

Phe Ala Gly Val Glu Asp Glu Lys His Lys Trp Lys Tyr Thr Asp Ile  
100 105 110

Glu Lys Leu Asn Ser Phe Pro Pro Asp Ser Glu Glu Gln Gln Ala Leu  
115 120 125

Ile Thr Ala Ile Gln Asp Glu Asp Gly Tyr Asn Trp Gly Tyr Asn Pro  
130 135 140

Val Leu Trp Gly Val Pro Lys Gly Ser Tyr Ala Gly Asn Ala Asn Gly  
145 150 155 160

Pro Cys Arg Ile